

SEQUENCE LISTING

<110> KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKY  
USHIO, Shimpei  
TORIGOE, Kakuji  
TANIMOTO, Tadao  
OKAMURA, Haruki  
KURIMOTO, Masashi  
FUKUDA, Shigeharu  
KUNIKATA, Toshio  
TANIGUCHI, Mutsuko  
KOHNO, Keizo

<120> INTERFERON- $\gamma$  INDUCING POLYPEPTIDE, PHARMACEUTICAL  
COMPOSITION THEREOF, MONOCLONAL ANTIBODY THERETO, AND  
METHODS OF USE

<130> USHIO=2

<140> NOT YET ASSIGNED

<141> 2000-11-21

<150> 08/832,198

<151> 1997-04-08

<150> 08/721,018

<151> 1996-09-26

<150> 08/558,191

<151> 1995-11-15

<150> 08/832,180

<151> 1997-04-08

<150> 08/558,818

<151> 1995-11-15

<150> 08/832,177

<151> 1997-04-08

<150> 08/599,879

<151> 1996-02-14

<150> 08/974,469

<151> 1996-02-14

<160> 22

<170> PatentIn Ver. 2.0

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<213> MOUSE

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Gln Ser Asp Leu Ile Phe Phe Gln Lys  
20 25

<210> 2

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Gln Pro Val Phe Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu  
1 5 10 15

Pro Gln

<210> 3

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<222> (1)..(471)

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<223> Xaa is methionine or threonine

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Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn  
1 5 10 15

gac caa gtt ctc ttc gtt gac aaa aga cag cct gtg ttc gag gat atg 96  
Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met  
20 25 30

act gat att gat caa agt gcc agt gaa ccc cag acc aga ctg ata ata 144  
 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile  
 35 40 45

tac atg tac aaa gac agt gaa gta aga gga ctg gct gtg acc ctc tct 192  
 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser  
 50 55 60

gtg aag gat agt aaa ayt tct acc ctc tcc tgt aag aac aag atc att 240  
 Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile  
 65 70 75 80

tcc ttt gag gaa atg gat cca cct gaa aat att gat gat ata caa agt 288  
 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser  
 85 90 95

gat ctc ata ttc ttt cag aaa cgt gtt cca gga cac aac aag atg gag 336  
 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu  
 100 105 110

ttt gaa tct tca ctg tat gaa gga cac ttt ctt gct tgc caa aag gaa 384  
 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu  
 115 120 125

gat gat gct ttc aaa ctc att ctg aaa aaa aag gat gaa aat ggg gat 432  
 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp  
 130 135 140

aaa tct gta atg ttc act ctc act aac tta cat caa agt 471  
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 145 150 155

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 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn  
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Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met  
 20 25 30

Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile  
 35 40 45

Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser  
50 55 60

Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile  
65 70 75 80

Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser  
85 90 95

Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu  
100 105 110

Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu  
115 120 125

Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp  
130 135 140

Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser  
145 150 155

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1 5 10 15

gac caa gtt ctc ttc att gac caa gga aat cgg cct cta ttt gaa gat 96  
Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
20 25 30

atg act gat tct gac tgt aga gat aat gca ccc cgg acc ata ttt att 144  
Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
35 40 45

ata agt atg tat aaa gat agc cag cct aga ggt atg gct gta act atc 192  
 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
 50 55 60

tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt gag aac aaa att 240  
 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile  
 65 70 75 80

att tcc ttt aag gaa atg aat cct cct gat aac atc aag gat aca aaa 288  
 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
 85 90 95

agt gac atc ata ttc ttt cag aga agt gtc cca gga cat gat aat aag 336  
 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
 100 105 110

atg caa ttt gaa tct tca tca tac gaa gga tac ttt cta gct tgt gaa 384  
 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
 115 120 125

aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa gag gat gaa ttg 432  
 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
 130 135 140

ggg gat aga tct ata atg ttc act gtt caa aac gaa gac 471  
 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
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Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
 20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
 35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
 50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile

65

70

75

80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
100 105 110

Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
145 150 155

&lt;210&gt; 7

&lt;211&gt; 1120

&lt;212&gt; DNA

&lt;213&gt; HUMAN

&lt;220&gt;

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&lt;222&gt; (178)..(756)

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&lt;223&gt; Xaa is isoleucine or threonine

&lt;400&gt; 7

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tggctgctaa agcggctgcc acctgctgca gtctacacag cttcggaag aggaaaggaa 120

cctcagacct tccagatcgc ttctctcgc aacaaactat ttgtcgcagg aataaag 177

atg gct gct gaa cca gta gaa gac aat tgc atc aac ttt gtg gca atg 225  
Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
1 5 10 15

aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac 273  
Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
20 25 30

ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata 321  
Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
35 40 45

aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct 369  
 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
 50 55 60

cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg 417  
 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
 65 70 75 80

acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg 465  
 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
 85 90 95

gct gta act atc tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt 513  
 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys  
 100 105 110

gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc 561  
 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile  
 115 120 125

aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga 609  
 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly  
 130 135 140

cat gat aat aag atg caa ttt gaa tct tca tca tac gaa gga tac ttt 657  
 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe  
 145 150 155 160

cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa 705  
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys  
 165 170 175

gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa 753  
 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu  
 180 185 190

gac tagctatttaa aatttcacgc cgggcgcagt ggctcacgcc tgtaatccca 806  
 Asp

gccctttggg aggctgaggc gggcagatca ccagaggtca ggtgttcaag accagcctga 866

ccaacatggt gaaacctcat ctctactaaa aatactaaaa attagctgag tgtagtgacg 926

catgccctca atcccagcta ctcaagaggc tgaggcagga gaatcacttg cactccggag 986

gtagagggtg tggtgagccg agattgcacc attgcgctct agcctgggca acaacagcaa 1046

aactccatct caaaaaataa aataaataaa taaacaaata aaaaattcat aatgtgaaaa 1106

aaaaaaaaaa aaaa

1120

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5

10

15

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn

20

25

30

Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile

35

40

45

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro

50

55

60

Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg

65

70

75

80

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met

85

90

95

Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys

100

105

110

Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile

115

120

125

Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly

130

135

140

His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe

145

150

155

160

Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys

165

170

175

Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu

180

185

190

Asp



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<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:UNKNOWN

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20

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<212> DNA  
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<220>  
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ttygargaya tgacngayat

20

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<213> Unknown

<220>  
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<212> DNA  
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<220>  
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26

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<213> Unknown

<220>

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26

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<211> 10

<212> PRT

<213> HUMAN

<400> 14

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser

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5

10

<210> 15

<211> 10

<212> PRT

<213> HUMAN

<400> 15

Ser Ile Met Phe Thr Val Gln Asn Glu Asp

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<210> 16

<211> 14

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Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg

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5

10

<210> 17

<211> 17

<212> PRT

<213> HUMAN

<400> 17

Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr  
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Lys

<210> 18

<211> 50

<212> PRT

<213> HUMAN

<400> 18

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
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Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
35 40 45

Ile Ser  
50

<210> 19

<211> 13

<212> PRT

<213> HUMAN

<400> 19

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg  
1 5 10

<210> 20

<211> 11

<212> PRT

<213> Artificial Sequence

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<210> 21

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

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34

<210> 22

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

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27